Meta-analysis — an introduction

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Acknowledging SIH



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The continued acknowledgment of the use of SIH facilities ensures the sustainability of our services.

Suggested wording for use of workshops and workflows:

"The authors acknowledge the Statistical workshops and workflows provided by the Sydney Informatics Hub, a Core Research Facility of the University of Sydney."

What is a workflow?

- Every statistical analysis is different, but all follow similar paths. It can be useful to know what these paths are
- We have developed practical, step-by-step instructions that we call 'workflows', that can you can follow and apply to your research
- We have a general research workflow that you can follow from hypothesis generation to publication
- And statistical workflows that focus on each major step along the way (e.g. experimental design, power calculation, model building, analysis using linear models/survival/multivariate/survey methods)



Statistical Workflows

- Our **statistical workflows** can be found within our workshop slides
- Statistical workflows are software agnostic, in that they can be applied using any statistical software
- There may also be accompanying software workflows that show you how to perform the statistical workflow using particular software packages (e.g. R or SPSS). We won't be going through these in detail during the workshop. If you are having trouble using them, we suggest you attend our monthly Hacky Hour where SIH staff can help you.



During the workshop



Ask short questions or clarifications during the workshop (either by Zoom chat or verbally). There will be breaks during the workshop for longer questions.



Slides with this blackboard icon are mainly for your reference, and the material will not be discussed during the workshop.



Challenge questions will be encountered throughout the workshop.



General Research Workflow

- 1. **Hypothesis Generation** (Research/Desktop Review)
- 2. Experimental and Analytical Design (sampling, power, ethics approval)
- 3. Collect/Store Data
- 4. Data cleaning
- 5. Exploratory Data Analysis (EDA)
- 6. Data Analysis aka inferential analysis
- 7. Predictive modelling
- 8. Publication













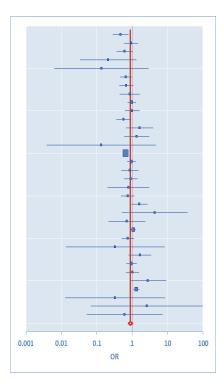






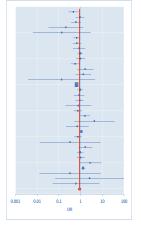
Outline

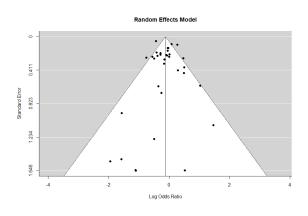
- The research context
- Meta-analysis workflow
- Meta-analysis concepts
- Software options
- Worked example using metafor in R
- Recap



Workshop Aims

Understand the key concepts and tools in meta-analysis





- Follow the steps to perform a meta-analysis
- Basic knowledge of performing these steps using a software package (metafor in R)

The research context

Meta analysis statistical workflow and software



Systematic Review - the research context

Narrative Review

This is generally what we see in a review article or in the first chapter of a research thesis. The aim is often to provide an <u>overview</u> rather than focussing on a single research question.

- Often subject to biases, in both selection and interpretation of studies, in order to fit a <u>narrative</u>.
- Methodology for surveying the topic and criteria for inclusion in the review are not defined.
- The studies might be treated differently according to the reviewer's assessment of their quality, however, this assessment will likely be subjective and unstated.
- Reasons for different findings are difficult to explore or resolve.

Systematic Review - the research context

Systematic Review

This aims to be a more objective review of a research topic.

- The research question is focussed and defined.
- Methodology for surveying the topic (e.g. databases, keywords) and criteria for inclusion in the review are defined in a protocol (eg PRISMA <u>prisma-statement.org</u>)
- Decisions on study inclusion, including assessing the quality of the studies, are considered to be more objective (e.g. GRADE)
- Information is extracted from the studies in a consistent manner.
- A meta-analysis (synthesis or combination of the data) is preceded by the systematic review. A meta-analysis doesn't always follow a systematic review.

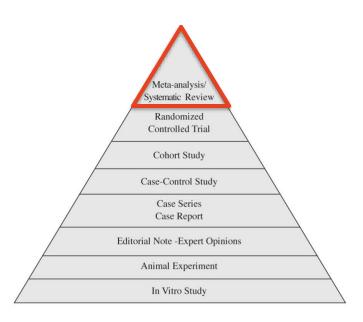
Systematic Review - the research context

Why choose to do Systematic Review and meta-analysis?

A well conducted meta-analysis sits at the top of the evidence pyramid

The results will be more generalisable than any single study

Evidence pyramid for medical studies



Systematic review – step by step overview

- 1. Formulate your research question
- 2. Develop eligibility criteria
- 3. Search the literature
- 4. Screen the literature, assessing the quality of studies
- 5. Extract the data
- 6. Synthesize and interpret the results
 - Meta-analysis
- 7. Publish and disseminate the results

The University of Sydney library guides

Literature Review - Library support



- The USyd library is the best place to get support on the wider questions of Literature Review and Systematic Review
- Resources available at the <u>Library Subject Guides: Systematic</u> <u>Review</u> and <u>Library Services</u>
- Library has dedicated support staff eligible staff and students can request a consultation with an <u>Academic Liaison Librarian</u>
- Workshops run through the year include "Getting started with Literature Review" – check the workshops calendar (filter category by "systematic review")
- <u>Canvas</u> OLE modules available online Writing a Literature Review OLEO5130

Workflow

Meta-analysis workflow



Meta Analysis – concepts and workflow step by step

Meta-Analysis workflow steps

- 1. Import the data (into the software)
- 2. Calculate Effect Size
- 3. Meta-Analysis summary (Fixed-Effect and Random-Effects)
- 4. Explore Heterogeneity (Q statistic, I², tau)
- 5. Publication bias (Funnel plot)
- 6. Sub-group analysis and/or meta-regression (if warranted)

1. Import the data Roles of Variables

What type of data do we have?

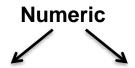
A variable – any factor or measure that can vary.

Explanatory (Independent) Variables – For example,

- Something that is set as part of the experimental design (e.g. control group and treatment group).
- Factors in the experimental subjects that may be relevant to the study (e.g. age and sex).

Response/Outcome (Dependent) Variables – these are measured or observed to determine whether they vary in response to the explanatory variables.

1. Import the data Types of variables



Continuous

(ratio or interval)

- Weight/height
- Blood pressure
- Time
- Plasma glucose levels

Discrete (count)

- Number of myocardial infarctions
- Size of litter
- Number of visits to a cage corner.



Ordinal

- Survey feedback
- Disease stages
- Pain descriptions

Nominal/binomial

- Eye colour
- Occupation
- Smoker/nonsmoker
- Present/absent
- Success/fail

The type of variable will influence what type of effect size is appropriate.

1. Import the data Study questions

Because of the analysis methods, meta-analyses primarily address quite simple comparisons.

- 1. Continuous variable (e.g. weight loss) measured in two groups.
- 2. Binary events (e.g. myocardial infarction [heart attack] yes/no)
- 3. Correlation between two continuous variables (e.g. blood lead levels in children and IQ scores).

More complex analyses may look at the influence of a modifying factor(s) i.e. a categorical variable (subgroup effect) or continuous variable (meta-regression).

The types of variables and the study design determine the type of effect size that is synthesized in the meta-analysis.

1. Import the data Study questions

Similarity of Studies

The studies included for meta-analysis will generally be of one type only, for example:

- 1. Studies where the treatment is assigned (eg RCT)
- 2. Observational studies no assignment to groups

They should be similar in such a way as to relate to the specific research question (refer back to steps 1 and 2 of the systematic review).

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for example (from Borenstein Ch 40)
What is the effect of an intervention? \rightarrow Randomised controlled trials
What is the cause of a rare disease? \rightarrow Case-control studies
What is the prevalence of a condition? \rightarrow Cross sectional studies
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2. Calculate Effect Size

Types - Difference in means

This is common when the explanatory variable is categorical and the response variable is numeric.

Example:

The study question is a comparison of the effectiveness of low fat diets vs low carbohydrate diets for weight loss

Explanatory variable is <u>diet type</u> – categorical (<u>low fat or low carbohydrate</u>). Response variable is <u>weight loss</u> – numeric (kg). The effect size is the difference in mean weight loss between the two groups.

$$Effect \ size = \bar{x}_{LF} - \bar{x}_{LC}$$

2. Calculate Effect Size

Types – proportions and Risk Ratio

These are typically used where you have 2 independent groups with a binary outcome.

Example: The study question is a comparison of survival rates in males and females at risk of myocardial infarctions (MI)

Explanatory variable is binary (sex: male/female)
Response variable is binary (survival: alive/dead)
p1 = proportion of females dying from MI
p2 = proportion of males dying from MI

Risk Difference Effect size = p1 - p2

Computations are carried out on the raw differences in proportions.

Another effect size (depending on the study design) is Risk Ratio

Risk Ratio Effect size = p1/p2

Computations are carried out on the natural log of the Risk Ratio.

2. Calculate Effect Size Types - Odds Ratio

The same outcome can also be expressed as an Odds Ratio.

	Death (event)	Survival (no event)	Proportion (Risk)	Odds
Female	а	b	p1=a/(a+b)	a/b
Male	С	d	p2=c/(c+d)	c/d

Odds Ratio Effect size
$$=\frac{a/b}{c/d} = \frac{ad}{bc}$$

When the risk of the event (eg death) is low, then the Odds Ratio will be similar in value to the Risk Ratio.

Analysis of an OR effect size is often preferred to RR because of superior statistical properties.

Computations are performed on the natural log of the odds ratio.

2. Calculate Effect Size Odds Ratio - combining



Suppose we want to combine Study A and B

Study	OR	
Α	2.0	
В	4.0	
Average(A:B)		

What is the average odds ratio of A and B?

2. Calculate Effect Size Odds Ratio - combining



Suppose we want to combine Study A and B

Study	OR	In(OR)
A	2.0	0.693
В	4.0	1.386
Average(A:B)		

What is the average odds ratio of A and B?

2. Calculate Effect Size Odds Ratio - combining



Suppose we want to combine Study A and B

Study	OR	In(OR)
Α	2.0	→ 0.693
В	4.0	→ 1.386
Average(A:B)	2.83 ←	1.040

To get the average odds ratio, you have to go via the log odds ratio

2. Calculate Effect Size

Types - Correlation

This is common when both variables are numeric.

Example:

Blood lead levels in children and IQ scores.

Both variables are numeric (IQ score and plasma lead concentration). We use the correlation coefficient.

$$Effect \ size \quad r = \frac{\sigma^2}{\sigma_x \sigma_y}$$

2. Calculate Effect Size

Types - Correlation

Like with Odds Ratios, combining correlation coefficients needs to be done using the right scale. In this case we use the Fisher's Z transformation

$$z = \frac{1}{2} ln \left(\frac{1+r}{1-r} \right)$$
 and back transform $r = \frac{exp(2z)-1}{exp(2z)+1}$

Study	(Pearson's) r	(Fisher's) z
Α	0.20	→ 0.2027
В	0.40	→ 0.4236
Average (A:B)	0.3033 ←	— 0.3132

2. Calculate Effect Size Combining Effect Sizes - considerations

Why not simply average the effect sizes from multiple studies?

There are a few things to consider

- 1. Standardisation
- 2. Weighting
- 3. Different types of effect sizes.

2. Calculate Effect Size

Standardised effect sizes

It may or may not be necessary to use standardised effect sizes.

Example 1: Selected studies examining effects of a supplement on fasting glucose levels may always measure the plasma glucose concentration.

Combine without standardisation

<u>Example 2</u>: Selected studies might examine ratings of anxiety among carers of people living with dementia vs matched control individuals. Some studies used the Generalised Anxiety Disorder Questionnaire (GAD-7), while other studies used the Hamilton Anxiety Rating Scale (HAM-A).

Standardise before combining

Standardised effect sizes are a way to transform effect sizes into a form where they can be compared and summarised.

2. Calculate Effect Size

Standardised effect sizes — difference in means

Many standardised effect sizes were defined by Jacob Cohen (1923-98). For example, Cohen's d

$$d = \frac{\overline{x_1} - \overline{x_2}}{s}$$

Where
$$S = \sqrt{\frac{[(n_1-1)s_1^2 + (n_2-1)s_2^2]}{(n_1+n_2-2)}}$$
 (the pooled within group SD)

Cochrane reviews refer to the "Standardised Mean Difference" (SMD) and use a variation of d, called Hedges' (adjusted) g.

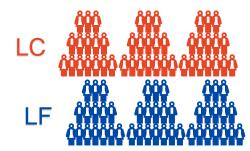
$$g = \left(1 - \frac{3}{4df - 1}\right)d$$
 df=n₁+n₂-3

2. Calculate Effect Size Weighting

Example:

The study question examines weight loss in a low carbohydrate diet (LC) vs a low fat (LF) diet.

Study 2 The difference in weight loss was 7.0 kg. The number of participants was 50 in each dietary group.



Should each study contribute equally to the calculation of the overall effect size? Is the overall effect size a <u>8.0 kg</u> weight loss?

2. Calculate Effect Size Weighting

- We need to consider the precision of the estimates for each study
- Sample size is a key component of study precision
- Studies that are more precise should have more weighting in the summary estimate
- Information about study precision is found in the Standard Error

2. Calculate Effect Size What is a standard error?

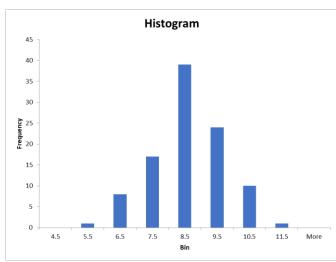
It is a measure of the precision of an estimate for a parameter.

Most commonly we think of the standard error of the mean.

Simulation: A sample of n=100 drawn from a normally distributed population with:

Population true mean
$$\mu = 8$$

Population true SD $\sigma = 1$



2. Calculate Effect Size What is a standard error?

Standard Error of the Mean is the standard deviation of the sample means

$$SEM = \frac{s}{\sqrt{n}}$$

For the example:
$$SEM = \frac{1.038}{\sqrt{100}} = 0.104$$

Sample Mean \bar{X} =8.111 **estimates** True mean μ = 8.000

with a standard error of 0.104

The standard error tells us about the precision of the estimate.

2. Calculate Effect Size What is a standard error?

Increasing the sample size reduces the standard error of the mean (because the denominator, \sqrt{n} , is larger).

Increasing the sample size will also reduce the standard error of the effect size.

Standard error for difference in means effect size

Difference in means = $\bar{x}_1 - \bar{x}_2$

pooled SD,
$$s = \sqrt{\frac{[(n_1 - 1)s_1^2 + (n_2 - 1)s_2^2]}{(n_1 + n_2 - 2)}}$$

Standard Error for Effect Size =
$$s\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}$$

Standard error for difference in means effect size

We want to weight the studies with a smaller standard error more relative to studies with a larger standard error...

...so we use the **inverse variance weight** or weighting factor (w) which is inverse to the effect size variance (i.e. the square of the standard error)

$$w = \frac{1}{SE^2}$$

Using weighting factors to combine effect sizes

$$\overline{ES} = \frac{\sum (w_i ES_i)}{\sum w_i}$$

The weighted mean effect size can then be calculated by summing the individual weighted effect sizes and dividing by the sum of the weighting factors.

Using weighting factors to combine effects sizes

LF vs LC diets for weight loss

Study 1: (small) n=10

$$ES_1=\bar{x}_{LC}-\bar{x}_{LF}=9.0kg$$
 , SD=2.9, therefore $SE=\frac{2.9}{\sqrt{10}}=0.917$ and $w_1=\frac{1}{SE^2}=\frac{1}{0.917^2}=1.189$

Study 2: (large) n=50

$$ES_2 = \bar{x}_{LC} - \bar{x}_{LF} = 7.0 kg$$
 , SD=2.9, therefore $SE = \frac{2.9}{\sqrt{50}} = 0.410$ and $w_2 = \frac{1}{9.4192} = \frac{1}{9.4192} = 5.945$

$$\overline{ES} = \frac{(w_1.ES_1) + (w_2.ES_2)}{(w_1 + w_2)} = \frac{(1.189x9) + (5.945x7)}{(1.189 + 5.945)}$$

Summary Effect Size,
$$\overline{ES} = \underline{7.3 \text{ kg}}$$

Example of a different effect size – log Odds Ratio

	Outcome 1	Outcome 2	Odds
Exposure 1	а	b	a/b
Exposure 2	С	d	c/d

$$ES_{LOR} = ln\left(\frac{ad}{bc}\right)$$

$$SE_{LOR} = \sqrt{\frac{1}{a} + \frac{1}{b} + \frac{1}{c} + \frac{1}{d}}$$

Weighting factor for Log OR

$$w_{LOR} = \frac{1}{SE^2} = \frac{abcd}{ab(c+d) + cd(a+b)}$$

Studies reporting different types of effect sizes

Research question

Is lead exposure, as measured by plasma lead concentrations, associated with the IQ of children?

1. Study type A

The lead was measured in the plasma of children and their IQ was tested.

Two continuous variables (plasma concentration and IQ)

Effect size – correlation

2. Study type B

The lead concentration in the plasma of children was used to classify the children into two groups – lead exposed and unexposed – and the IQ of the children was tested.

One categorical (explanatory) variable (lead exposure) One continuous (outcome) variable (IQ)

Effect size – difference in means

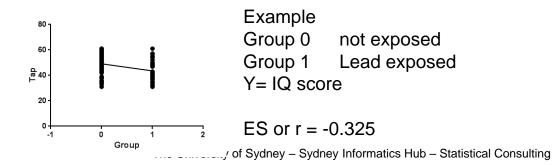
Studies reporting different types of effect sizes

Choices

- 1. Do analysis on different types of effect sizes separately
- 2. Use methods to estimate one type of effect size from another

For example:

The Point-Biserial Correlation is a special case of the Pearson's Correlation Coefficient. It is used when one variable is continuous and the other variable is categorical (binomial). For the categorical outcome, one exposure or outcome is assigned 0 and the alternative outcome or exposure is assigned 1.



2. Calculate Effect Size Studies reporting different types of effect sizes

2. Use methods to estimate one type of effect size from another

These methods are an approximation and introduce more complexity and uncertainty in determining effect sizes.

For example, a Point-Biserial Correlation is often an underestimate of a correlation coefficient using two continuous variables

Note: Studies that use different measures may differ in other substantive ways. This needs to be considered.

Extracting the effect size from other information

In a perfect world...

Standardised effect size for difference in means between two groups, its SE and the weighting factor would be calculated from these values.

Group	n	Mean	SD
Α	34	42.4	6.7
В	28	34.6	2.8

However, it is possible to estimate the standardised effect size from a t statistic or a p value. Eg.

Cohen's
$$d = t_{(n_A + n_B - 2)} \sqrt{\frac{1}{n_A} + \frac{1}{n_B}}$$

Occasionally, non-significant results get reported in insufficient detail for effect size calculation/estimation.

2. Calculate Effect Size Extracting Effect Sizes



Another situation when effect sizes can be difficult to determine is from a multivariable analysis.

The regression model might contain the explanatory variable of interest, however, its relationship with the response variable is adjusted by the presence of other explanatory variables in the model.

It is difficult to extract an effect size when only partial regression weights are presented without any kind of univariate analysis.

2. Calculate Effect Size Estimating the true effect size?

Understanding the (true) mean effect size is assisted by:

- 1. Weighting effect sizes when calculating a mean effect size.
- 2. Calculating a confidence interval for the mean effect size.
- 3. Exploring the heterogeneity of the effect sizes and considering different models for the effect sizes (see step 4).

Estimating the true effect size?

2. Calculating a confidence interval for the mean effect size.

The 95% Confidence Interval for a mean effect is calculated so that 95% of the time* the interval contains the population effect size.

It is calculated from the standard error of the mean effect size.

$$SE_{\overline{ES}} = \sqrt{\frac{1}{\sum w_i}}$$

The SE is multiplied by the critical z value representing the desired confidence level (z=1.96 for 95%).

95% CI for
$$\overline{ES} = \overline{ES} \pm 1.96 * SE_{\overline{ES}}$$

If the 95% CI does not contain 0 then there is a statistically-significant effect at $\alpha=0.05$.

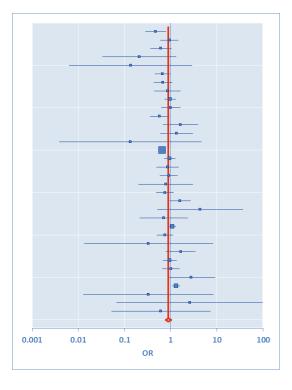
* If you repeated the meta-analysis 100 times (and had different primary studies for each – unlikely in reality) – on average 95 times the CI would contain the true population effect size

3. Meta-Analysis summary

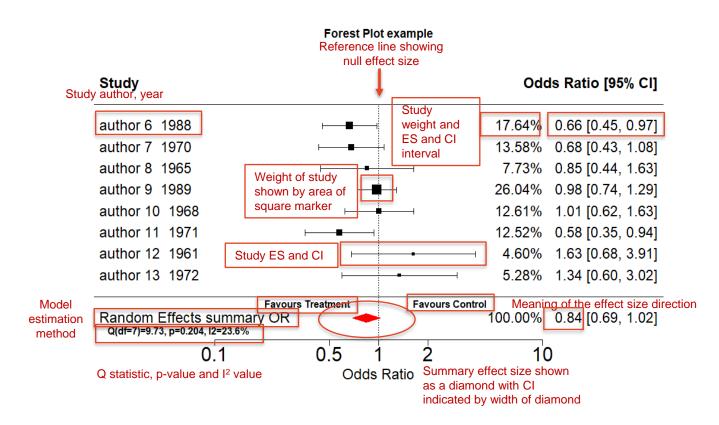
The meta-analysis summary combines all the information we have put together on the study effect sizes, the summary effect size, their associated uncertainties, and information about their spread (or heterogeneity)

The Forest plot is a common tool for displaying this information.

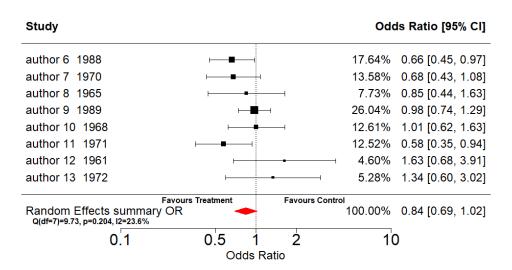
The name refers to the "forest" of lines produced.



3. Meta-Analysis summary Forest Plot







Do these individual study effect sizes estimate the same underlying true effect size?

4. Explore Heterogeneity Fixed-Effect Models

This model assumes there is one underlying population effect size. The variation in individual effect sizes is due to random sampling.

For example, the population effect of a low fat diet (compared to LC diet) is a weight loss of 8 kg.

Due to random sampling error, the individual studies show an effect size ranging from 6 to 10 kg.

The true effect size is 8 kg. If we had infinitely large sample sizes for each study, then we would have ES=8.0 every time, and the standard errors would be zero.

4. Explore Heterogeneity Fixed-Effect Models

Is it reasonable to assume the distribution of observed effect sizes is from a population with a single effect size?

Why?

Why not?

Assumption of Homogeneity – Q statistic

The homogeneity test is based on the (Cochran's) Q statistic

$$Q = \sum_{i=1}^{k} w_i (ES_i - \overline{ES})^2$$

The Q statistic has a chi-square distribution with k-1 degrees of freedom where k is the number of effect sizes (studies).

If the observed Q statistic is over the critical value (producing a p value less than α) then the null hypothesis (homogeneity of effect sizes) is rejected.

Quantifying heterogeneity with the I² statistic

Effect sizes are always going to be heterogeneous. Why not quantify the inconsistency rather than test with some arbitrary cut-off?

A common approach is to apportion the amount of variation due to heterogeneity in study effect sizes and the amount of variation due to sampling error.

$$I^2 = 100\% \times \left(\frac{Q - df}{Q}\right)$$

 I^2 conveys the amount of variation in the effects sizes that would remain if we could remove sampling error.

Quantifying heterogeneity with the I² statistic

What is a large l^2 value?

Rules of thumb:

from Borenstein:

- 25% is low
- 50% is moderate
- 75% is high

From Cochrane Training:

- 0% to 40%: might not be important
- 30% to 60%: may represent moderate heterogeneity
- 50% to 90%: may represent substantial heterogeneity
- 75% to 100%: considerable heterogeneity

4. Explore Heterogeneity Random Effects models

This model assumes that there are differences in the underlying effect sizes whose sources cannot be identified.

Therefore the variation in effects sizes is due to sampling error (as with fixed effect models) but with an additional component that estimates other sources of variability.

$$v_{RE} = v_{\theta} + v_{i}$$

Where

 v_i is the estimate of the variance associated with sampling error. v_{θ} is the estimate of the between-studies variance, also known as tau-squared (τ^2).

4. Explore Heterogeneity Random Effects models

 v_{θ} is the estimate of the between-studies variance, also known as tau-squared (τ^2).

The calculation of τ^2 can get technical. The simplest model for tau-squared is the "DerSimonian and Laird" method.

Other options for τ^2

- REML is the default option in the metafor package
- The Knapp-Hartung adjustment to the summary effect confidence interval is commonly used with random effects models as well.
- For dichotomous data (like Odds Ratio) the Mantel-Haenszel method is an alternative estimation method.
- For a general discussion of the methods refer to the Cochrane Handbook section 10.10.4.4



The consequences of using a Random Effects Model

The inverse variance weights calculated previously (and thus the mean effect sizes) assumed the fixed effect model.

inverse variance weight =
$$\frac{1}{SE^2}$$

However, with the random effects model that becomes

$$inverse \ variance \ weight = \frac{1}{v_{RE}}$$

Therefore, when switching to a random effects model, all mean effect sizes and confidence intervals are recalculated.

A commonly used approach

Approach the analysis using the fixed effect model as the default model and explore the heterogeneity of the effects sizes using a statistical test (Q statistic).

- 1. The test for heterogeneity is not significant therefore a fixed effect model is consistent with the data and this model is used; OR
- 2. The test for heterogeneity is significant so the analysis is repeated with the random effects model.

The problem with this approach...

The non-significant p value does not prove the null hypothesis (that there is one true effect size).

It is recommended that the decision is based on rigorous assumptions regarding the sample of studies.

How should we select a statistical model?

The choice of a statistical model should depend on the sampling frame that was used to select studies for the analysis. If we are working with one population, then we should use the fixed-effect model. If we are working with a universe of populations, we should use the random-effects model. Consider the following two cases.

Case 1. A pharmaceutical company plans to enroll 1,000 patients. Because the staff can only work with 100 patients at time, it randomly divides the patients into 10 groups of 100 patients, and runs the identical study with each. We know all studies are based on the same population, since that's how we selected them. The fixed-effect model matches the way the studies were sampled.

Case 2. We locate a series of published studies that were performed by different people in different locations at different times. While the studies all looked at similar interventions, it stands to reason that the true impact of this intervention will differ from study to study. If the studies were conducted in different hospitals it's likely that the patient population (age, co-morbid diseases) varied from one hospital to the next, and that the intervention was therefore more effective in some hospitals than in others. It's also possible that the intervention itself (the precise dosage, length of follow-up from one hospital to the next and that this could have an impact on the effect size. While the agreence

Reference: metaanalysis.com

4. Explore Heterogeneity Prospective Meta-analysis

Cochrane Methods



"A prospective meta-analysis (PMA) is a meta-analysis in which studies (usually randomised controlled trials) are identified, evaluated and determined to be eligible <u>before</u> the results of any of the studies become known. PMA can help to overcome some of the recognised problems of retrospective meta-analyses."

This approach may lead to low heterogeneity and a justifiable assumption of a Fixed Effect model

N

Fixed-Effect and Random-Effects summary

- A fixed-effect meta-analysis estimates a single effect that is assumed to be common to every study, while a random-effects meta-analysis estimates the mean of a distribution of effects.
- Study weights are more balanced under the random-effects model than under the fixedeffect model. Large studies are assigned less relative weight and small studies are assigned
 more relative weight as compared with the fixed-effect model.
- The standard error of the summary effect and (it follows) the confidence intervals for the summary effect are wider under the random-effects model than under the fixed-effect model.
- The selection of a model must be based solely on the question of which model fits the distribution of effect sizes, and takes account of the relevant source(s) of error. When studies are gathered from the published literature, the random effects model is generally a more plausible match.
- The strategy of starting with a fixed-effect model and then moving to a random-effects model if the test for heterogeneity is significant is a mistake, and should be strongly discouraged.

Borenstein et. al., 2009

4. Explore Heterogeneity Selecting a model

A random effects model would fit most types of meta-analyses, based on the sources of studies.

At first glance, the random effects model would appear to be the more conservative approach.

However...

Random effects incorporate the between study variance into the denominator of each weight. This has the effect of weighting the studies more evenly and can lead to the effect size being shifted towards the effect size of smaller studies.

Perhaps not a problem unless there is a <u>different effect size</u> observed among the smaller studies compared to the larger studies.

How can this be assessed?

5. Publication Bias and other sources of bias



Selection bias

Only choose studies which they are familiar with or support their view-point

Occurs when the two groups being compared differ systematically, eg. differences in the characteristics between those who are selected for a study.

Performance bias

differences between groups in the care that is provided, or in exposure to factors other than the interventions of interest.

Detection bias

differences between groups in how outcomes are determined.

Attrition bias

differences between groups in withdrawals from a study.

Reporting bias

differences between reported and unreported findings.

Publication bias

Only select studies which have been published. In general, studies with statistically significant or positive results are more likely to be published than those with non-significant or negative results.

Language bias

Only select studies written in English

Indexing bias

Only search a limited number of databases or use a limited choice of search terms.

5. Publication Bias



"The small proportion of results chosen for publication are unrepresentative of scientists' repeated samplings of the real world." Young, loannidis & Al-Ubaydli, PLOS Medicine, doi:10.1371

"The winner's curse refers to the phenomenon that studies that find evidence of an effect often provide inflated estimates of the size of that effect. Such inflation is expected when an effect has to pass a certain threshold — such as reaching statistical significance — in order for it to have been 'discovered'. Effect inflation is worst for small, low-powered studies, which can only detect effects that happen to be large."

Button et al, Nature Reviews Neuroscience, 2013,14:365

5. Publication Bias



A review by Easterbrook et al quantified the extent of the problem in clinical research

Easterbrook, P.J et al. "Publication Bias in Clinical Research." The Lancet (British edition) 337.8746 (1991): 867–872. Web.

https://sydney.primo.exlibrisgroup.com/permalink/61USYD_INST/2rsddf/cdi_scopus_primary_21140048

5. Publication Bias what can you do?

- As individuals, we can't change the forces that cause publication bias.
- Look at studies that are available from other sources and may be more representative.
- Research Grey Literature sources
- Avoid indexing bias! (a more thorough literature search will generate a more valid meta-analysis)

5. Publication Bias Funnel Plot

A funnel plot is a scatter plot of each study's Effect Size vs a measure of the study's size or precision e.g. SE of the effect size.

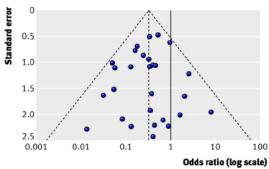


Fig 1 Example of symmetrical funnel plot. The outer dashed lines indicate the triangular region within which 95% of studies are expected to lie in the absence of both biases and heterogeneity (fixed effect summary log odds ratio±1.96×standard error of summary log odds ratio). The solid vertical line corresponds to no intervention effect

Sterne, Jonathan A C et al. "Recommendations for Examining and Interpreting Funnel Plot Asymmetry in Meta-Analyses of Randomised Controlled Trials." BMJ 343.7818 (2011): c4737–307. Web.

5. Publication Bias Funnel Plot Asymmetry

It has been observed that small studies report larger effect sizes compared with large studies. This may be due to publication bias but could also be due to other factors e.g. different subgroups in the smaller studies.

A different effect size in the small studies can be observed as asymmetry in the funnel plot.

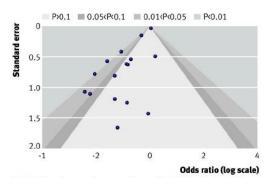


Fig 4 Contour enhanced funnel plot for trials of the effect of intravenous magnesium on mortality after myocardial infarction

5. Publication Bias Test for funnel plot asymmetry

It is possible to test for asymmetry but check the recommendations as it may not be advisable.

For example,

- The minimum number of studies should be substantially greater than 10.
- The asymmetry test should not be used if the studies are of similar size/precision.
- The plots need to be considered in the context of the other characteristics of the studies.

If there is significant asymmetry, the effect estimate should be compared under the fixed and random-effects model as the random effects model might be skewing the mean effect size towards the smaller studies.

Refer to the Cochrane Handbook <u>section 13.3.5.2</u> for further advice.

5. Publication Bias Funnel Plot Asymmetry

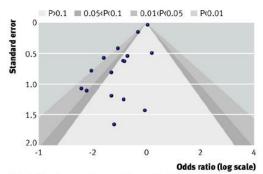


Fig 4 Contour enhanced funnel plot for trials of the effect of intravenous magnesium on mortality after myocardial infarction

One very large study showing no beneficial effect of intervention and other small studies showing mostly beneficial effect.

Fixed Effect model – No net effect

Random Effects model – An overall beneficial effect

This is because the missing study data (RHS of plot) results in a smaller between study variance than should be the case.

6. Sub-group analysis moderating factor

1. There is one underlying population effect size. The variation in individual effect sizes is due to random sampling.

For example, the population effect of a low fat diet (compared to LC diet) is a weight loss of 8 kg.

Due to random sampling error, the individual studies show an effect size ranging from 7 to 9 kg.

OR

2. There is variation in the population effect sizes but this is systematic and due to a moderating factor.

For example, the population effect of the LF diet on weight loss is 7.5 kg in <u>older adults</u> whilst the effect is 8.5 kg in <u>younger adults</u>.

6. Sub-group analysis moderating factor

If we suspect a moderating factor is present (and we have the data for it)...

...then the homogeneity analysis can be partitioned according to the grouping factor.

For example,

The categorical or grouping variable is Age Group (older adults or younger adults).

The Q statistic is partitioned into the portion that is explained by Age Group (Q_B) and the residual portion that explains the within group variation (Q_W) .

$$Q = Q_B + Q_W$$

6. Sub-group analysis Meta-regression



Meta-regression is a more flexible approach to understanding the factors that might contribute to an effect size because:

- The moderator can be a numeric variable instead of being restricted to a categorical variable.
- Multiple variables (including categorical variables when coded appropriately) can be considered in the same analysis.

Example: Weight loss for LF diet (vs LC diet)

Rather than compare sub-groups for younger vs older adults, if we had information on subject age on a continuous scale then we could incorporate this covariate in a meta-regression model. [However, take care to consider issues such as aggregation/ecological bias! - see <u>Cochrane 10.11.5.5</u>]

Like all multiple regression models, a large ratio of subjects (i.e. studies) to covariates is required (suggestion of 10:1).

The regression model can be formulated using the assumptions of the fixed or random effects model.

Recap

Meta analysis statistical workflow and software



Meta-Analysis workflow

So just to re-cap, here are the basic workflow steps we went through:

- 1. Import the data
- 2. Calculate Effect Size
- 3. Meta-Analysis summary (Fixed-Effect and Random-Effects)
- 4. Explore Heterogeneity (Q statistic, I², tau)
- 5. Publication bias (Funnel plot)
- 6. Sub-group analysis and/or meta-regression (if warranted)

Meta Analysis software

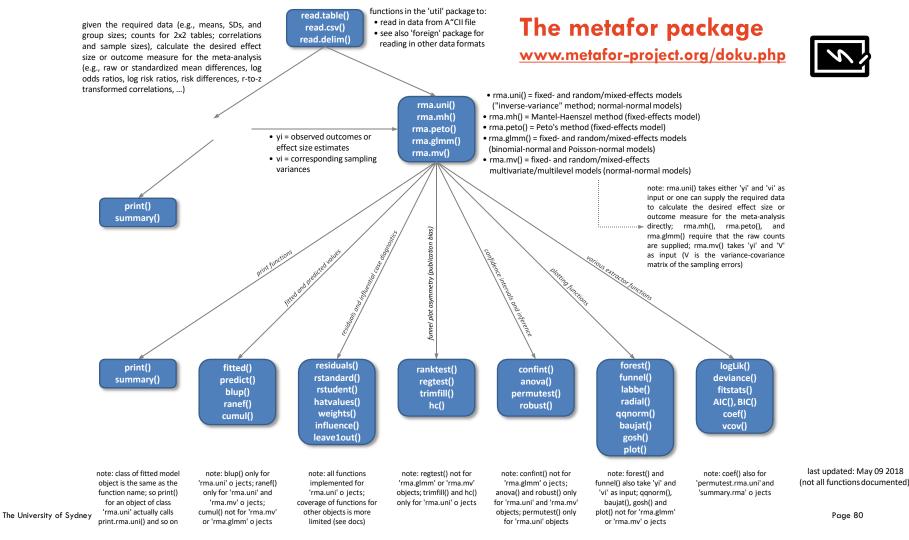
Name, URL	Comment	Interface
SPSS	From version 28	GUI
STATA https://www.stata.com/new-in-stata/meta-analysis/	From version 16	Command meta
CMA www.meta-analysis.com	Developed by Borenstein (world expert). Costs \$\$. Popular	GUI
MIX https://www.meta-analysis-made-easy.com/	Add-In for Excel (Windows), user friendly, Modest \$	Excel menus
Revman https://training.cochrane.org/onl ine-learning/core-software- cochrane-reviews/revman	Open-source (free) from Cochrane Training Web and Desktop versions	GUI

There are of course other options not listed here...

Meta Analysis in R

Software or package	Origin	Comments
meta	Schwarzer, 2007	General package, easy to use
metafor	Viechtbauer, 2010	General package with extensive functionality
netmeta	Schwarzer & Rücker, 2015	Add-on package for meta to allow network meta-analysis
dmetar	Harrer, et al, 2021	Example datasets and extra functions to work with meta, metafor, netmeta and gemtc
metap	Dewey, 2020	Enables meta-analysis using significance values
mada	Doebler, 2020	Meta-Analysis of Diagnostic Accuracy (for summary ROC)
jamovi https://www.jamovi.org/	uses metafor R package	User friendly interface, can save R script

Viechtbauer recently estimated there are 152 meta-analysis packages available for R!



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Worked example

Met analysis with metafor in R



Example: Meta analysis with metafor in R Sutton-Smith Cholesterol lowering intervention on mortality

This data is taken from the book "<u>Methods of Meta-analysis in Medical</u> <u>Research</u>" by A. J. Sutton

(originally extracted from the article: Smith, George Davey, Fujian Song, and Trevor A Sheldon. "Cholesterol Lowering and Mortality: The Importance of Considering Initial Level of Risk." British Medical Journal 306.6889 (1993): 1367—. Print.)

The data comprises 34 studies assessing the effectiveness of cholesterol treatments on mortality in randomised controlled trials.

Example: Meta analysis with metafor in R Sutton-Smith Cholesterol lowering intervention on mortality

The following files are provided for you to follow this example on your own device:

The data: Meta_Sutton_Smith.csv

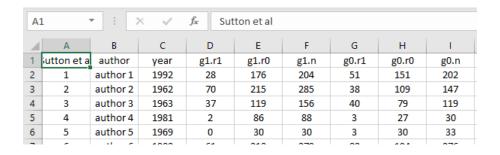
The R script: Meta-Analysis workshop example.R

If you are not an R user, just follow the output. A similar workflow can be followed using other software tools.

Step 1: Import the data

We have the data in a csv file ready to read in using:

metadata <- read.csv("Meta_Sutton_Smith.csv", header = T)</pre>



Step 1: Import the data

These studies compare the mortality rates for Group 1 (intervention) and Group 0 (control).

The data is presented in counts where r1=event, r0=no event, n=total

				Group			Group			
•	Sutton.et.al [‡]	author [‡]	year [‡]	g1.r1 [‡]	g1.r0 [‡]	g1.n [‡]	g0.r1 [‡]	g0.r0 [‡]	g0.n [‡]	
1	1	author 1	1992	28	176	204	51	151	202	
2	2	author 2	1962	70	215	285	38	109	147	
3	3	author 3	1963	37	119	156	40	79	119	
4	4	author 4	1981	2	86	88	3	27	30	
5	5	author 5	1969	0	30	30	3	30	33	
6	6	author 6	1988	61	218	279	82	194	276	
7	7	author 7	1970	41	165	206	55	151	206	
8	8	author 8	1965	20	103	123	24	105	129	
9	9	author 9	1989	111	907	1018	113	902	1015	
10	10	author 10	1968	81	346	427	27	116	143	

What are the explanatory and response variables? Describe...

Step 2: Calculate effect size (Odds Ratios)

We use the "escalc" function from metafor to create "yi" which is the log OR effect size and "vi" which is the variance of "yi".

meta.es <- escalc(measure = "OR", g1.r1, g1.r0, g0.r1, g0.r0, data = metadata, slab = paste(author, year, sep = ", "))

										ţ	ţ
_	Sutton.et.al	author	year [‡]	g1.r1 [‡]	g1.r0 [‡]	g1.n [‡]	g0.r1 [‡]	g0.r0 [‡]	g0.n	yi [‡]	vi [‡]
1	1	author 1	1992	28	176	204	51	151	202	-0.752825281	0.067626464
2	2	author 2	1962	70	215	285	38	109	147	-0.068381064	0.054426978
3	3	author 3	1963	37	119	156	40	79	119	-0.487637182	0.073088616
4	4	author 4	1981	2	86	88	3	27	30	-1.563975538	0.881998277

Step 3: Calculate meta-analysis summary

We use the "rma" function from metafor to create the meta-analysis summary statistics

Random effects is the default meta.re <- rma(yi, vi, data = meta.es)

Fixed effect requires an optional argument meta.fe <- rma(yi, vi, data = meta.es, method = "FE")

Step 3: Calculate meta-analysis summary

Random-Effects model

```
Note default REML
                                                                       estimation
Random-Effects Model (k = 34; tau<sup>2</sup> estimator: REML)
tau^2 (estimated amount of total heterogeneity): 0.0478 (SE = 0.0269)
tau (square root of estimated tau^2 value):
                                                 0.2186
I^2 (total heterogeneity / total variability):
                                                53.87%
HA2 (total variability / sampling variability): 2.17
Test for Heterogeneity:
Q(df = 33) = 89.1065, p-val < .0001
Model Results:
                                  ci.lb ci.ub
estimate
                     zval
                             p∨al
              se
                                                               Information on the summary
 -0.1178 0.0628 -1.8750 0.0608 -0.2410 0.0053
                                                               effect size as log(OR)
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Step 3: Calculate meta-analysis summary Fixed-Effect model

Step 3: Calculate meta-analysis summary

Model comparison (convert log(OR) to OR first)

meta.re.or <- exp(c(meta.re\$b, meta.re\$ci.lb, meta.re\$ci.ub))

meta.fe.or <- exp(c(meta.fe\$b, meta.fe\$ci.lb, meta.fe\$ci.ub))

Model	Effect size	lower CI	Upper Cl	p value
Random-Effects	0.889	0.786	1.005	0.0608
Fixed-Effect	0.844	0.793	0.900	<.0001

Random-Effects model has

Reduced OR Effect size from 0.84 to 0.89 (closer to 1)

- Increased width of CI from $0.79 \sim 0.90$ to $0.79 \sim 1.01$

CI for effect size now traverses 1.00 (just)

Step 3: Calculate meta-analysis summary

Forest Plot – R code

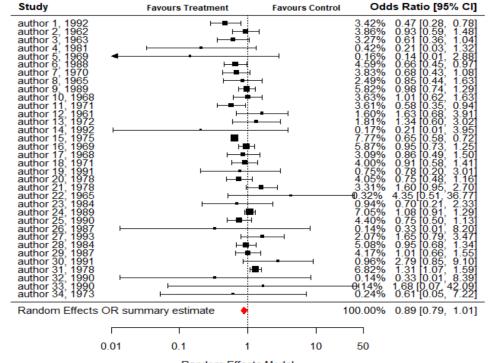
Use the forest() function to produce the plot. You may need to adjust quite a few plotting parameters to get it just the way you want. This is the code I used for the fixed-effect forest plot (code for random not shown).

```
forest(
 meta.fe,
 header = TRUE,
 atransf = exp, #display OR on x-axis log scale
 at = log(c(0.01, 0.1, 1, 10, 50)),
 x \lim = c(-8, 8),
 xlab = "Fixed-Effect Model",
 mlab = "Fixed-Effect OR summary estimate",
 showweights = TRUE,
 pch = 15,
 border = "red", #colour of summary diamond border
 col = "red", #colour of summary diamond fill
 main = "The effect of cholesterol lowering interventions \n on mortality \n Sutton-Smith data"
op <- par(cex = 0.75, font = 2)
text(c(-2, 2), 36, c("Favours Treatment", "Favours Control"))
par(op)
```

Step 3: Calculate metaanalysis summary

Forest Plot – Random-Effects

The effect of cholesterol lowering interventions on mortality Sutton-Smith data

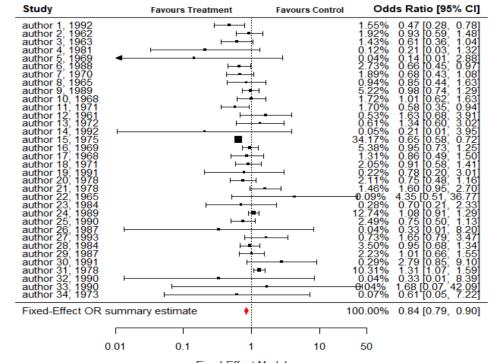


The University of Sydney Random Effects Model Page 92

Step 3: Calculate metaanalysis summary

Forest Plot – Fixed-Effect

The effect of cholesterol lowering interventions on mortality Sutton-Smith data



Step 3: Calculate meta-analysis summary

Forest Plot

Comments

- Note estimates and Cl's for each study. Each study's weight designated by size of square.
- Graphical representation of (moderate) heterogeneity.
- Weightings are different between the two models

Step 4: Explore heterogeneity

- Q statistic is significant p<0.0001 (heterogeneous studies)
- I squared (proportion of inconsistency) 54%~63% is moderate
- Tau squared estimate is > zero
- We expect studies to have underlying differences in effect size
- We should use random effects

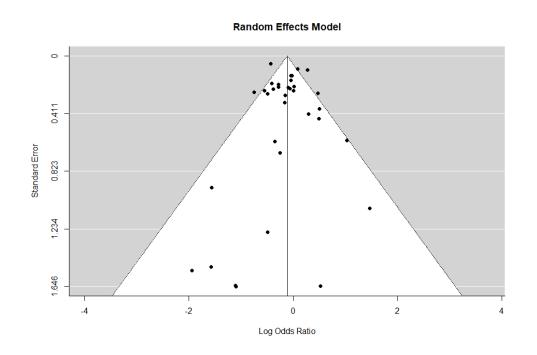
Step 5: Publication Bias -

Funnel Plot

funnel(meta.re, main = "Random Effects Model")

Check for asymmetry

- No of studies > 10
- Studies are of various sizes and precision
- Plot appears to be symmetrical (can use random effects model without problem)
- One more check

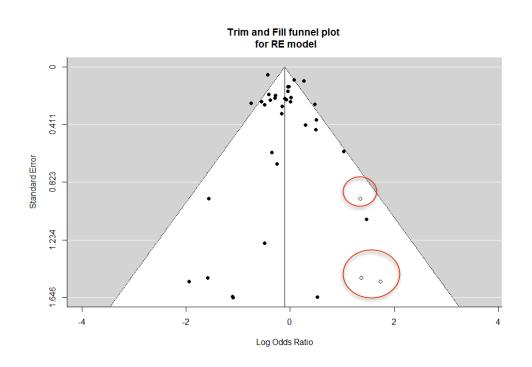


Step 5: Publication Bias

Funnel Plot

Use trimfill() function to add imputed studies to the funnel plot meta.tf <- trimfill(meta.re) funnel(meta.tf, main = "Trim and Fill funnel plot \n for RE model")

Note: 3 imputed studies (open circles)



Step 6: Sub-group analysis

The original study looked at a sub-group analysis using the factor:

Coronary heart disease risk group – high, medium, low

Sub-group analysis found significant differences between these groups, with only the high risk CHD (treatment) group showing a benefit in terms of total mortality.

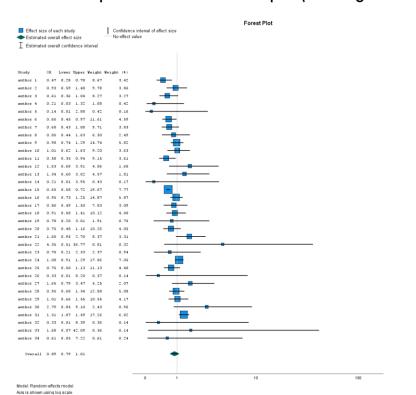
A meta-regression was also carried out showing a similar trend.

(This analysis is not included in this workshop)

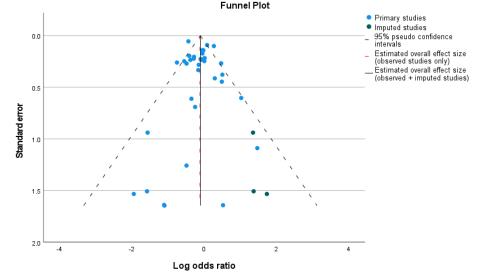
SPSS (Version 28) Meta-Analysis

SPSS will produce the same output (although there are fewer formatting options)

Random Effects estimate







Recap

Challenge questions and additional resources





Q1: You are performing a meta-analysis on differences in quality of life between an intervention and a control group. Some studies measure quality of life with WHOQOL and other studies use EuroQuol. What should you do?

- a) Analyse all the studies together
- b) Choose to analyse only WHOQOL or EuroQuol, whichever has the most studies
- c) Standardise before combining
- d) Check that WHOQOL and EuroQuol both measure what you want, then if yes, apply step (c).



Q1: You are performing a meta-analysis on differences in quality of life between an intervention and a control group. Some studies measure quality of life with WHOQOL and other studies use EuroQuol. What should you do?

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- Q2: The main purpose of the funnel plot is to:
- a) Show which studies should be included in the meta-analysis
- b) Show which studies show a positive or negative effect
- c) Show whether publication bias might be present
- d) Show the effect size estimates and confidence intervals

9

- Q2: The main purpose of the funnel plot is to:
- a) Show which studies should be included in the meta-analysis
- b) Show which studies show a positive or negative effect
- c) Show whether publication bias might be present
- d) Show the effect size estimates and confidence intervals



Q3: In comparison with a Fixed-effect model, a Random-effects model will

- A. Apply larger weights to smaller studies
- B. Be accompanied by an estimate of tau squared
- C. Account for underlying variation in the effect size across studies
- D. All of the above



Q3: In comparison with a Fixed-effect model, a Random-effects model will

- A. Apply larger weights to smaller studies
- B. Be accompanied by an estimate of tau squared
- C. Account for underlying variation in the effect size across studies
- D. All of the above

Published Meta-analysis examples



When publication bias is present – from Experimental Psychology (inspect the funnel plot)

Shanks, David R et al. "Romance, Risk, and Replication: Can Consumer Choices and Risk-Taking Be Primed by Mating Motives?" Journal of experimental psychology. General 144.6 (2015): e142–e158. Web.

https://sydney.primo.exlibrisgroup.com/permalink/61USYD_INST/1367smt/cdi_gale_infotracacademiconefile_A444328766

2. Good example of tabulation of study data (Tables 1,2,3) but bad example of plotting meta-regression (figures 2 and 4)

Rong, Chen. "Egg Consumption and Risk of Coronary Heart Disease and Stroke: Dose-Response Meta-Analysis of Prospective Cohort Studies." BMJ: British Medical Journal 346.7890 (2013): 12–12. Web.

https://sydney.primo.exlibrisgroup.com/permalink/61USYD_INST/1367smt/cdi_proquest_miscellaneous_1273301943

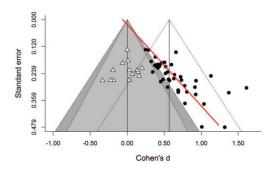


Figure 2. Funnel plot from the meta-analysis. Black circles represent the

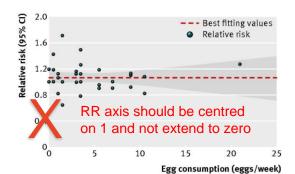


Fig 2 Dose-response analyses of egg consumption and

Published Meta-analysis examples



3. Scientific fraud and retracted papers examined by sub-group analysis

Zarychanski, Ryan et al. "Association of Hydroxyethyl Starch Administration With Mortality and Acute Kidney Injury in Critically III Patients Requiring Volume Resuscitation: A Systematic Review and Meta-Analysis." JAMA: the journal of the American Medical Association 309.7 (2013): 678–688. Web.

https://sydney.primo.exlibrisgroup.com/permalink/61USYD_INST/1367smt/cdi_proquest_miscellaneous_1291608126

4. Good example of Cumulative metaanalysis over 17yr

Rizos, Ntzani. "Association Between Omega-3 Fatty Acid Supplementation and Risk of Major Cardiovascular Disease Events: A Systematic Review and Meta-Analysis." JAMA: the journal of the American Medical Association 308.10 (2012): 1024–1033. Web.

https://sydney.primo.exlibrisgroup.com/permalink/61USYDINST/1367smt/cdi proquest miscellaneous 1039344012

Retraction Watch

Tracking retractions as a window into the scientific process

Figure 5. Cumulative Meta-analysis of the Omega-3 Supplements for All-Cause Mortality

	Cumulative Sample Size	RR (95% CI)		Favors Omega-3 PUFAs	Favors Control
Sacks et al,27 1995	59	0.30 (0.01-7.13)	-		
Leng et al, ²⁶ 1998	179	0.79 (0.20-3.20)	-		
Marchioli et al,1 1999	11 503	0.86 (0.77-0.97)			
von Schacky et al,25 1999	11726	0.86 (0.77-0.97)			
Nilsen et al, ²⁴ 2001	12326	0.87 (0.77-0.97)			
Leaf et al,34 2005	12728	0.87 (0.78-0.98)			
Raitt et al,33 2005	12928	0.86 (0.77-0.97)			
Brouwer et al.35 2006	13474	0.86 (0.77-0.96)			
Svensson et al,32 2006	13680	0.87 (0.78-0.97)			
Yokovama et al.3 2007	32 325	0.94 (0.84-1.06)			
Tavazzi et al,2 2008	39300	0.94 (0.88-0.99)			
Garbagnati et al,38 2009	39338	0.94 (0.87-1.00)		-	
Kromhout et al.4 2010	44 175	0.94 (0.89-1.00)		-	
Einvik et al,37 2010	44738	0.94 (0.88-1.01)		-	
Rauch et al. 36 2010	48542	0.96 (0.88-1.04)			
Galan et al. ²⁹ 2010	50743	0.96 (0.89-1.03)		-	-
ORIGIN,5 2012	63279	0.96 (0.91-1.02)		-	-
			0.5	1.	.0 2
				Relative Ris	k (95% CI)

Error bars indicate the 95% CI of the cumulative meta-analysis estimates as randomized patients accumulate through time. PUFAs indicates polyunsaturated fatty acids; RR, relative risk.

Additional Resources



For Systematic Review:

- University Library Library Guide for Systematic Review
- University Library Workshops, Canvas modules and Consultations
- Cochrane Handbook for Systematic Reviews of Interventions Online version

For Meta-Analysis:

- Borenstein, Michael. Introduction to Meta-Analysis. Chichester, U.K: John Wiley & Sons, 2009. Print.
- Cochrane Handbook Chapter 10: Meta-Analyses Online version
- Cochrane online learning http://training.cochrane.org/online-learning
- Hartung, Joachim, Guido Knapp, and Bimal K Sinha. <u>Statistical Meta-Analysis with Applications</u>.
 Aufl. Hoboken, N.J.: Wiley-Interscience, 2008. Web.
- Schwarzer, Guido., James R. Carpenter, and Gerta. Rücker. <u>Meta-Analysis with R</u>. 1st ed. 2015. Cham:
 Springer International Publishing, 2015. Web.
- A guide to Prospective Meta-analysis (from USyd NHMRC CTC)
 https://www.bmj.com/content/367/bmj.I5342.short

Further Assistance at Sydney University

SIH

- Statistical Consulting website: containing our workshop slides and our favourite external resources (including links for learning R and SPSS)
- Hacky Hour an informal monthly meetup for getting help with coding or using statistics software
- 1 on 1 Consults can be requested on our website (click on the big red 'contact us' link)

SIH Workshops

- Create your own custom programmes tailored to your research needs by attending more of our Statistical Consulting workshops. Look for the statistics workshops on <u>our training page.</u>
- Other SIH workshops
- Sign up to our mailing list to be notified of upcoming training

Other

- Open Learning Environment (OLE) courses
- Linkedin Learning

How to use our workshops

Workshops developed by the Statistical Consulting Team within the Sydney Informatics Hub form an integrated modular framework. Researchers are encouraged to choose modules to create custom programmes tailored to their specific needs. This is achieved through:

- Short 90 minute workshops, acknowledging researchers rarely have time for long multiday workshops.
- Providing statistical workflows appliable in any software, that give practical step by step instructions which researchers return to when analysing and interpreting their data or designing their study e.g. workflows for designing studies for strong causal inference, model diagnostics, interpretation and presentation of results.
- Each one focusing on a specific statistical method while also integrating and referencing the
 others to give a holistic understanding of how data can be transformed into knowledge
 from a statistical perspective from hypothesis generation to publication.

For other workshops that fit into this integrated framework refer to our training link page under statistics https://www.sydney.edu.au/research/facilities/sydney-informatics-hub/workshops-and-training.html#stats

We recommend our Experimental Design and Sample Size Workshops

Experimental Design Workshop

- Far too many researchers think they know all they need to in this area. We commonly see designs that could be substantially improved for stronger causal inference and improved results which leads to publication in higher impact journals (amongst other benefits).
- Even if you have already collected your data it is well worth attending since it may improve your write up and analysis e.g. we had a client who didn't realise they had a very strong Before/After Control/Impact (BACI) design.

Sample and Power Workshop

- Shows the steps and decisions researchers need to make when designing an experiments to ensure sufficient sample e.g. Power, minimum required to fit the necessary model, etc.
- Also how much Power the study has i.e. does it have sufficient power to detect the effects you expect to see, or is your study a complete waste of time and resources.



A reminder: Acknowledging SIH

All University of Sydney resources are available to Sydney researchers **free of charge**. The use of the SIH services including the Artemis HPC and associated support and training warrants acknowledgement in any publications, conference proceedings or posters describing work facilitated by these services.

The continued acknowledgment of the use of SIH facilities ensures the sustainability of our services.

Suggested wording for use of workshops and workflows:

"The authors acknowledge the Statistical workshops and workflows provided by the Sydney Informatics Hub, a Core Research Facility of the University of Sydney."

We value your feedback



We want to hear about you and whether this workshop has helped you in your research. What worked and what didn't work.

We actively use the feedback to improve our workshops.

Completing this survey really does help us and we would appreciate your help! It only takes a few minutes to complete (promise!)

You will receive a link to the anonymous survey by email